



SEQUENCE LISTING

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1127

TECH CENTER 1600/2900

<110> JOBLING, Stephen A.
National Starch and Chemical Company

<120> IMPROVEMENTS IN OR RELATING TO STARCH CONTENT OF PLANTS

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<140> US 09/297,703

<141> 1999-07-19

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 Cys Tyr Ser Ser Ser Thr Asp Gln Leu Glu Ala Pro Gly Thr Val Ser
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 95 100 105

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 Lys Ile Val Glu Asp Glu Val Asn Lys Glu Ser Val Pro Met Arg Glu
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 Thr Val Ser Ile Arg Lys Ile Gly Ser Lys Pro Arg Ser Ile Pro Pro
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770 775 780

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ctt ggc tac aat gct gtt cag atc atg gct att caa gag cat tcc tat Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr 350 355 360 365	1225
tat gct agt ttt ggg tac cat gtc aca aac ttt ttt gca cct agc agc Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser 370 375 380	1273
cga ttt gga act cct gat gat ttg aag tct tta ata gat aaa gct cat Arg Phe Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His 385 390 395	1321
gag tta ggg ctg ctt gtt ctc atg gat att gtt cat agc cat gcg tca	1369

Glu	Leu	Gly	Leu	Leu	Val	Leu	Met	Asp	Ile	Val	His	Ser	His	Ala	Ser		
		400					405					410					
aat	aat	acg	ttg	gat	ggg	ctg	aac	atg	ttt	gat	ggg	acg	gat	agt	cac	1417	
Asn	Asn	Thr	Leu	Asp	Gly	Leu	Asn	Met	Phe	Asp	Gly	Thr	Asp	Ser	His		
		415				420					425						
tac	ttc	cac	tcc	gga	tca	cgg	ggg	cat	cat	tgg	ttg	tgg	gac	tct	cgc	1465	
Tyr	Phe	His	Ser	Gly	Ser	Arg	Gly	His	His	Trp	Leu	Trp	Asp	Ser	Arg		
		430			435					440					445		
ctt	ttc	aac	tat	gga	agc	tgg	gag	gtg	cta	aga	ttt	ctt	ctt	tca	aat	1513	
Leu	Phe	Asn	Tyr	Gly	Ser	Trp	Glu	Val	Leu	Arg	Phe	Leu	Leu	Ser	Asn		
				450					455					460			
gca	aga	tgg	tgg	ttg	gaa	gag	tac	agg	ttt	gat	ggg	ttt	aga	ttt	gat	1561	
Ala	Arg	Trp	Trp	Leu	Glu	Glu	Tyr	Arg	Phe	Asp	Gly	Phe	Arg	Phe	Asp		
				465				470					475				
ggg	gtg	act	tcc	atg	atg	tac	act	ccc	cat	ggg	ttg	cag	gta	gct	ttt	1609	
Gly	Val	Thr	Ser	Met	Met	Tyr	Thr	Pro	His	Gly	Leu	Gln	Val	Ala	Phe		
		480					485					490					
act	ggc	aac	tac	aat	gag	tac	ttt	gga	tat	gca	act	gat	gta	gat	gct	1657	
Thr	Gly	Asn	Tyr	Asn	Glu	Tyr	Phe	Gly	Tyr	Ala	Thr	Asp	Val	Asp	Ala		
		495				500					505						
gtg	att	tat	ttg	atg	ctt	gtg	aat	gat	atg	att	cac	ggg	ctt	ttc	cct	1705	
Val	Ile	Tyr	Leu	Met	Leu	Val	Asn	Asp	Met	Ile	His	Gly	Leu	Phe	Pro		
					515					520					525		
gag	gct	gtt	acc	att	ggg	gaa	gat	gtt	agc	gga	aag	cca	aca	ttt	tgc	1753	
Glu	Ala	Val	Thr	Ile	Gly	Glu	Asp	Val	Ser	Gly	Lys	Pro	Thr	Phe	Cys		
				530					535					540			
att	cca	gtg	gaa	gat	ggg	ggg	gtt	gga	ttt	gat	tac	cgt	ctc	cac	atg	1801	
Ile	Pro	Val	Glu	Asp	Gly	Gly	Val	Gly	Phe	Asp	Tyr	Arg	Leu	His	Met		
			545					550					555				
gcc	att	gcc	gat	aaa	tgg	att	gag	att	ctt	aag	aag	aga	gat	gag	gac	1849	
Ala	Ile	Ala	Asp	Lys	Trp	Ile	Glu	Ile	Leu	Lys	Lys	Arg	Asp	Glu	Asp		
			560				565					570					
tgg	aaa	atg	ggg	gac	att	gtg	cat	aca	ctc	acc	aac	aga	agg	tgg	ttg	1897	
Trp	Lys	Met	Gly	Asp	Ile	Val	His	Thr	Leu	Thr	Asn	Arg	Arg	Trp	Leu		
		575				580					585						
gaa	aaa	tgt	gtt	gct	tat	gct	gaa	agt	cat	gac	caa	gct	ctt	gtt	ggg	1945	
Glu	Lys	Cys	Val	Ala	Tyr	Ala	Glu	Ser	His	Asp	Gln	Ala	Leu	Val	Gly		
		590			595					600				605			
gac	aaa	act	att	gca	ttt	tgg	ctg	atg	gac	aag	gac	atg	tac	gac	ttc	1993	
Asp	Lys	Thr	Ile	Ala	Phe	Trp	Leu	Met	Asp	Lys	Asp	Met	Tyr	Asp	Phe		
				610					615					620			

atg gct cgt gac aga cca tct act cct ctt ata gat cgt gga ata gca Met Ala Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala 625 630 635	2041
ttg cac aaa atg atc agg ctt att acc atg ggc tta ggc gga gaa gga Leu His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly 640 645 650	2089
tat ttg aat ttt atg gga aat gaa ttt gga cat cct gag tgg att gat Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp 655 660 665	2137
ttt cca aga ggg gat cga cat ctg ccc aat ggt aaa gta att cca ggg Phe Pro Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly 670 675 680 685	2185
aac aac cac agt tat gat aaa tgc cgt cgt aga ttt gat cta ggt gat Asn Asn His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp 690 695 700	2233
gca gac tat cta aga tat cat gga atg caa gag ttt gat cag gca atg Ala Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met 705 710 715	2281
caa cat ctt gaa gaa gcc tat ggt ttc atg act tct gag cac cag tat Gln His Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr 720 725 730	2329
ata tca cgg aag gat gaa gga gat cgg atc att gtc ttt gag agg gga Ile Ser Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly 735 740 745	2377
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tac cga gtt ggc tgc ttc aag tca gga aag tac aag att gtt ttg gac Tyr Arg Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp 770 775 780	2473
tcg gat gat ggc ttg ttt gga ggc ttc aac agg ctt agt cat gat gcc Ser Asp Asp Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala 785 790 795	2521
gag cac ttc acc ttt gac ggg tgg tat gat aac cgg cct cgg tcc ttc Glu His Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe 800 805 810	2569
atg gta tat gca cca tct agg aca gca gtg gtc tat gct tta gta gaa Met Val Tyr Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu 815 820 825	2617
gat gaa gag aat gaa gca gag aat gaa gta gaa agt gaa gtg aaa cca Asp Glu Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro 830 835 840 845	2665
gcc tcc ggc tga gatagatatt tagtaagagg atcccctaaa gcaggaatgg	2717

Ala Ser Gly

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Ser Gly Leu Ser Phe Leu Leu Lys Lys Glu Leu Phe Pro Arg Lys Ile
35 40 45

Phe Ala Gly Lys Ser Ser Tyr Glu Ser Asp Ser Ser Asn Leu Thr Val
50 55 60

Ser Ala Ser Glu Lys Val Leu Val Pro Asp Asp Gln Ile Asp Gly Ser
65 70 75 80

Ser Ser Ser Thr Tyr Gln Leu Glu Thr Thr Gly Thr Val Leu Glu Glu
85 90 95

Ser Gln Val Leu Gly Asp Ala Glu Ser Leu Val Met Glu Asp Asp Lys
100 105 110

Asn Val Glu Glu Asp Glu Val Lys Lys Glu Ser Val Pro Leu His Glu
115 120 125

Thr Ile Ser Ile Gly Lys Ser Glu Ser Lys Pro Arg Ser Ile Pro Pro
130 135 140

Pro Gly Ser Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser Leu Ala Gly
145 150 155 160

Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu Arg
165 170 175

Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe Ser Arg Gly
180 185 190

Phe Glu Lys Phe Gly Phe Leu Arg Ser Glu Thr Gly Ile Thr Tyr Arg
195 200 205

Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly Asp Phe Asn
210 215 220

Asn Trp Asn Pro Asn Ala Asp Val Met Thr Arg Asn Glu Phe Gly Val
225 230 235 240

Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile Pro
245 250 255

His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Ile Lys
260 265 270

Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly Glu
275 280 285

Ile Pro Tyr Asn Ala Ile Tyr Tyr Asp Pro Pro Lys Glu Glu Lys Tyr
290 295 300

Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr
305 310 315 320

Glu Ser His Val Gly Met Ser Ser Met Glu Pro Ile Ile Asn Thr Tyr
325 330 335

Ala Asn Phe Arg Asp Asp Met Leu Pro Arg Ile Lys Lys Leu Gly Tyr
340 345 350

Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser
355 360 365

Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly
370 375 380

Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly
385 390 395 400

Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn Thr
405 410 415

Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe His
420 425 430

Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe Asn
435 440 445

Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp
450 455 460

Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
465 470 475 480

Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly Asn
485 490 495

Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile Tyr
500 505 510

Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala Val
515 520 525

Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro Val
530 535 540

Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile Ala
545 550 555 560

Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys Met
565 570 575

Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys
580 585 590

Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr
595 600 605

Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Arg
 610 615 620

Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His Lys
 625 630 635 640

Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn
 645 650 655

Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg
 660 665 670

Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn His
 675 680 685

Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr
 690 695 700

Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu
 705 710 715 720

Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg
 725 730 735

Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val
 740 745 750

Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg Val
 755 760 765

Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp
 770 775 780

Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala Glu His Phe
 785 790 795 800

Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr
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Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu Asp Glu Glu
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<213> Artificial sequence

<223> conserved sequence in SBEII proteins

<213> Artificial sequence

<223> mature terminus of pea protein

<213> Artificial sequence

<223> predicted mature terminus of cassava SBEII protein

24